

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/S73/280
Source: IPWP
Date Processed by STIC: 4-4-06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/04/2006

PATENT APPLICATION: US/10/573,280

TIME: 10:40:42

Input Set : N:\DA\pto.da.txt

Output Set: N:\CRF4\04042006\J573280.raw

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3 <110> APPLICANT: Hutton, John C.
4     O'Brien, Richard
5     Davidson, Howard
6     Hackl, Seija
8 <120> TITLE OF INVENTION: Use of Islet Glucose-6-Phosphatase Related Protein as a
Diagnostic Tool
9     and Therapeutic Target for Autoimmune Diabetes
11 <130> FILE REFERENCE: 2848-56-PCT
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/573,280
C--> 13 <141> CURRENT FILING DATE: 2005-03-22
13 <150> PRIOR APPLICATION NUMBER: US 60/505317
14 <151> PRIOR FILING DATE: 2003-09-22
16 <160> NUMBER OF SEQ ID NOS: 7
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1068
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1065)
28 <223> OTHER INFORMATION:
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33 1          5          10          15
35 aag gac tac cga gct tac tac act ttt cta aat ttt atg tcc aat gtt      96
36 Lys Asp Tyr Arg Ala Tyr Tyr Thr Phe Leu Asn Phe Met Ser Asn Val
37          20          25          30
39 gga gac ccc agg aat atc ttt ttc att tat ttt cca ctt tgt ttt caa      144
40 Gly Asp Pro Arg Asn Ile Phe Phe Ile Tyr Phe Pro Leu Cys Phe Gln
41          35          40          45
43 ttt aat cag aca gtt gga acc aag atg ata tgg gta gca gtc att ggg      192
44 Phe Asn Gln Thr Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly
45          50          55          60
47 gat tgg tta aat ctt ata ttt aaa tgg ata tta ttt ggt cat cga cct      240
48 Asp Trp Leu Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro
49 65          70          75          80
51 tac tgg tgg gtc caa gaa act cag att tac cca aat cac tca agt cca      288
52 Tyr Trp Trp Val Gln Glu Thr Gln Ile Tyr Pro Asn His Ser Ser Pro
53          85          90          95
55 tgc ctt gaa cag ttc cct act aca tgt gaa aca ggt cca gga agt cca      336
56 Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro
57          100          105          110

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59 tct ggc cat gca atg ggc gca tcc tgt gtc tgg tat gtc atg gta acc      384
60 Ser Gly His Ala Met Gly Ala Ser Cys Val Trp Tyr Val Met Val Thr
61      115      120      125
63 gct gcc ctg agc cac act gtc tgt ggg atg gat aag ttc tct atc act      432
64 Ala Ala Leu Ser His Thr Val Cys Gly Met Asp Lys Phe Ser Ile Thr
65      130      135      140
67 ctg cac aga ctg acc tgg tca ttt ctt tgg agt gtt ttt tgg ttg att      480
68 Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu Ile
69 145      150      155      160
71 caa atc agt gtc tgc atc tcc aga gta ttc ata gca aca cat ttt cct      528
72 Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe Pro
73      165      170      175
75 cat caa gtt att ctt gga gta att ggt ggc atg ctg gtg gca gag gcc      576
76 His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu Ala
77      180      185      190
79 ttt gaa cac act cca ggc atc caa acg gcc agt ctg ggc aca tac ctg      624
80 Phe Glu His Thr Pro Gly Ile Gln Thr Ala Ser Leu Gly Thr Tyr Leu
81      195      200      205
83 aag acc aac ctc ttt ctc ttc ctg ttt gca gtt ggc ttt ttc ctg ctt      672
84 Lys Thr Asn Leu Phe Leu Phe Leu Phe Ala Val Gly Phe Tyr Leu Leu
85      210      215      220
87 ctt agg gtg ctc aac att gac ctg ctg tgg tcc gtg ccc ata gcc aaa      720
88 Leu Arg Val Leu Asn Ile Asp Leu Leu Trp Ser Val Pro Ile Ala Lys
89 225      230      235      240
91 aag tgg tgt gct aac ccc gac tgg atc cac att gac acc acg cct ttt      768
92 Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Thr Thr Pro Phe
93      245      250      255
95 gct gga ctc gtg aga aac ctt ggg gtc ctc ttt ggc ttg ggc ttt gca      816
96 Ala Gly Leu Val Arg Asn Leu Gly Val Leu Phe Gly Leu Gly Phe Ala
97      260      265      270
99 atc aac tca gag atg ttc ctc ctg agc tgc cga ggg gga aat aac tac      864
100 Ile Asn Ser Glu Met Phe Leu Leu Ser Cys Arg Gly Gly Asn Asn Tyr
101      275      280      285
103 aca ctg agc ttc cgg ttg ctc tgt gcc ttg acc tca ttg aca ata ctg      912
104 Thr Leu Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Ile Leu
105      290      295      300
107 cag ctc tac cat ttc ctc cag atc ccg act cac gaa gag cat tta ttt      960
108 Gln Leu Tyr His Phe Leu Gln Ile Pro Thr His Glu Glu His Leu Phe
109 305      310      315      320
111 tat gtg ctg tct ttt tgt aaa agt gca tcc att ccc cta act gtg gtt      1008
112 Tyr Val Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Thr Val Val
113      325      330      335
115 gct ttc att ccc tac tct gtt cat atg tta atg aaa caa agc gga aag      1056
116 Ala Phe Ile Pro Tyr Ser Val His Met Leu Met Lys Gln Ser Gly Lys
117      340      345      350
119 aag agt cag tag      1068
120 Lys Ser Gln
121      355
124 <210> SEQ ID NO: 2

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Input Set : N:\DA\pto.da.txt

Output Set: N:\CRF4\04042006\J573280.raw

125 <211> LENGTH: 355

126 <212> TYPE: PRT

127 <213> ORGANISM: Homo sapiens

129 <400> SEQUENCE: 2

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132 1 5 10 15
135 Lys Asp Tyr Arg Ala Tyr Tyr Thr Phe Leu Asn Phe Met Ser Asn Val
136 20 25 30
139 Gly Asp Pro Arg Asn Ile Phe Phe Ile Tyr Phe Pro Leu Cys Phe Gln
140 35 40 45
143 Phe Asn Gln Thr Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly
144 50 55 60
147 Asp Trp Leu Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro
148 65 70 75 80
151 Tyr Trp Trp Val Gln Glu Thr Gln Ile Tyr Pro Asn His Ser Ser Pro
152 85 90 95
155 Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro
156 100 105 110
159 Ser Gly His Ala Met Gly Ala Ser Cys Val Trp Tyr Val Met Val Thr
160 115 120 125
163 Ala Ala Leu Ser His Thr Val Cys Gly Met Asp Lys Phe Ser Ile Thr
164 130 135 140
167 Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu Ile
168 145 150 155 160
171 Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe Pro
172 165 170 175
175 His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu Ala
176 180 185 190
179 Phe Glu His Thr Pro Gly Ile Gln Thr Ala Ser Leu Gly Thr Tyr Leu
180 195 200 205
183 Lys Thr Asn Leu Phe Leu Phe Leu Phe Ala Val Gly Phe Tyr Leu Leu
184 210 215 220
187 Leu Arg Val Leu Asn Ile Asp Leu Leu Trp Ser Val Pro Ile Ala Lys
188 225 230 235 240
191 Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Thr Thr Pro Phe
192 245 250 255
195 Ala Gly Leu Val Arg Asn Leu Gly Val Leu Phe Gly Leu Gly Phe Ala
196 260 265 270
199 Ile Asn Ser Glu Met Phe Leu Leu Ser Cys Arg Gly Gly Asn Asn Tyr
200 275 280 285
203 Thr Leu Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Ile Leu
204 290 295 300
207 Gln Leu Tyr His Phe Leu Gln Ile Pro Thr His Glu Glu His Leu Phe
208 305 310 315 320
211 Tyr Val Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Thr Val Val
212 325 330 335
215 Ala Phe Ile Pro Tyr Ser Val His Met Leu Met Lys Gln Ser Gly Lys
216 340 345 350
219 Lys Ser Gln

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Input Set : N:\DA\pto.da.txt

Output Set: N:\CRF4\04042006\J573280.raw

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220          355
223 <210> SEQ ID NO: 3
224 <211> LENGTH: 1901
225 <212> TYPE: DNA
226 <213> ORGANISM: Mus musculus
228 <220> FEATURE:
229 <221> NAME/KEY: CDS
230 <222> LOCATION: (63)..(1127)
231 <223> OTHER INFORMATION:
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236 ag atg gat ttc ctt cat agg agt gga gtg ctt att att cat cat ctg      107
237 Met Asp Phe Leu His Arg Ser Gly Val Leu Ile Ile His His Leu
238 1 5 10 15
240 cag gag gac tac cgg act tac tat ggt ttt cta aat ttt atg tcc aat      155
241 Gln Glu Asp Tyr Arg Thr Tyr Tyr Gly Phe Leu Asn Phe Met Ser Asn
242 20 25 30
244 gtt gga gac ccc cga aat atc ttt tct att tac ttc cca ctt tgg ttt      203
245 Val Gly Asp Pro Arg Asn Ile Phe Ser Ile Tyr Phe Pro Leu Trp Phe
246 35 40 45
248 cag ttg aat cag aat gtt gga acc aag atg atc tgg gta gcg gtc ata      251
249 Gln Leu Asn Gln Asn Val Gly Thr Lys Met Ile Trp Val Ala Val Ile
250 50 55 60
252 ggg gac tgg ttc aat ctc ata ttt aaa tgg ata ttg ttt ggc cat cgt      299
253 Gly Asp Trp Phe Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg
254 65 70 75
256 cct tac tgg tgg ata caa gaa act gag att tat cca aat cat tca agc      347
257 Pro Tyr Trp Trp Ile Gln Glu Thr Glu Ile Tyr Pro Asn His Ser Ser
258 80 85 90 95
260 cca tgt ctt gag cag ttt cct act acg tgt gaa aca ggc cca gga agt      395
261 Pro Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser
262 100 105 110
264 cca tct ggc cac gca atg ggc tca tgc tgc gtc tgg tat gtc atg gta      443
265 Pro Ser Gly His Ala Met Gly Ser Ser Cys Val Trp Tyr Val Met Val
266 115 120 125
268 aca gct gcc cta agc tac acc atc agc cgg atg gag gag tcc tct gtc      491
269 Thr Ala Ala Leu Ser Tyr Thr Ile Ser Arg Met Glu Glu Ser Ser Val
270 130 135 140
272 act ctg cac aga ctg acc tgg tcc ttt ctg tgg agt gtt ttc tgg ttg      539
273 Thr Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu
274 145 150 155
276 att caa atc agc gtc tgc atc tca aga gta ttc ata gcc aca cat ttc      587
277 Ile Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe
278 160 165 170 175
280 ccc cat cag gtc att ctt gga gtg att ggt ggg atg cta gta gcc gag      635
281 Pro His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu
282 180 185 190
284 gcc ttt gaa cac act cca gga gtc cac atg gcc agc ttg agt gtg tac      683
285 Ala Phe Glu His Thr Pro Gly Val His Met Ala Ser Leu Ser Val Tyr

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Input Set : N:\DA\pto.da.txt

Output Set: N:\CRF4\04042006\J573280.raw

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286          195          200          205
288 ctg aag acc aac gtc ttc ctc ttc ctg ttt gcc ctc ggc ttt tac ctg      731
289 Leu Lys Thr Asn Val Phe Leu Phe Leu Phe Ala Leu Gly Phe Tyr Leu
290          210          215          220
292 ctt ctc cga ctg ttc ggt att gac ctg ctg tgg tcc gtg ccc atc gcc      779
293 Leu Leu Arg Leu Phe Gly Ile Asp Leu Leu Trp Ser Val Pro Ile Ala
294          225          230          235
296 aaa aag tgg tgt gcc aac cca gac tgg atc cac att gac agc acg cct      827
297 Lys Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Ser Thr Pro
298 240          245          250          255
300 ttt gct gga ctc gtg aga aac ctc ggg gtc ctc ttt ggc ttg ggt ttc      875
301 Phe Ala Gly Leu Val Arg Asn Leu Gly Val Leu Phe Gly Leu Gly Phe
302          260          265          270
304 gcc atc aac tca gaa atg ttc ctt cgg agc tgc cag gga gaa aat ggc      923
305 Ala Ile Asn Ser Glu Met Phe Leu Arg Ser Cys Gln Gly Glu Asn Gly
306          275          280          285
308 acc aag ccg agc ttc cgc ttg ctc tgt gct ctg acc tca ctg acc aca      971
309 Thr Lys Pro Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Thr
310          290          295          300
312 atg caa ctt tat cgc ttc atc aag atc ccg act cac gcg gaa cct tta      1015
313 Met Gln Leu Tyr Arg Phe Ile Lys Ile Pro Thr His Ala Glu Pro Leu
314          305          310          315
316 ttt tac ctg ttg tct ttc tgt aaa agt gcg tcc atc ccc ctg atg gtg      1067
317 Phe Tyr Leu Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Met Val
318 320          325          330          335
320 gtg gct cta att ccc tac tgt gta cat atg tta atg aga ccc ggt gac      1115
321 Val Ala Leu Ile Pro Tyr Cys Val His Met Leu Met Arg Pro Gly Asp
322          340          345          350
324 aag aag act aaa tagagctgca gtgccctgtg gtctgaggat cacctacttt      1167
325 Lys Lys Thr Lys
326          355
328 ctgttttctt caatagagcc acagcacaga gactgggagc gtctctacag aggtcacacc      1227
330 atgatgacca aaggtcctgc tccaccacaca gacatgttta gtctgctttc caagtggcat      1287
332 ttaaaaaata acagtattta accagaaaagt ccatattttc ttgacaaaac tgacaatacg      1347
334 gtaacatatg agagatggta taacccatgt aaagacagtt gacaggggct ggatgcttac      1407
336 attccagtta gcagaaagac tccttctaata catagtattt agcagtcaac aaaacccccca      1467
338 ggagctgatg tttctatcat cttaaagtct ggctacttca ggctcctgtg gaccacttag      1527
340 aagtgaccac ggtctacttt tacttttagg agtcaattct ttcaaaattc tcatgtatca      1587
342 gataaggaaa tagaggtttg ttcagatcaa gtaacttgac tgtaatagtg cagggttgaa      1647
344 accagagttg gaacacaagg cttctgatac atatatctct ataagaatgc tttctttctt      1707
346 tctttttagg gagttaaaaa aaaagagcaa atgcatgtat ttaaaatcta tgtttgccat      1767
348 ctaaaacacc catcttttca gaaatggcat tgggaatgcta cattctgctt gacttatgct      1827
350 cagagtacag tgtcttttcc aggctagcaa tggctgtata tatttcaata aacgctgctg      1887
352 aaaacaaccc actg      1901
355 <210> SEQ ID NO: 4
356 <211> LENGTH: 355
357 <212> TYPE: PRT
358 <213> ORGANISM: Mus musculus
360 <400> SEQUENCE: 4

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/573,280

DATE: 04/04/2006
TIME: 10:40:43

Input Set : N:\DA\pto.da.txt
Output Set: N:\CRF4\04042006\J573280.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 2,5,10,13 ✓

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/573,280

DATE: 04/04/2006

TIME: 10:40:43

Input Set : N:\DA\pto.da.txt

Output Set: N:\CRF4\04042006\J573280.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28
L:233 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:231
L:485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0